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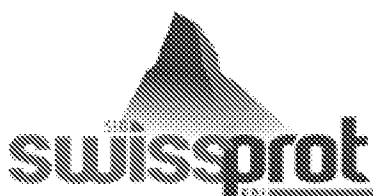
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ID DLK2_HUMAN Reviewed; 383 AA.
AC Q6UY11; Q5T3T8; Q9BQ54;
DT 25-OCT-2004, integrated into UniProtKB/Swiss-Prot.
DT 05-JUL-2004, sequence version 1.
DT 22-JUL-2008, entry version 48.
DE RecName: Full=Delta-like protein 2;
DE AltName: Full=EGF-like domain-containing protein 9;
DE AltName: Full=Multiple EGF-like domain protein 9;
DE Flags: Precursor;
GN Name=DLK2; Synonyms=EGFL9; ORFNames=UNQ2903/PRO28633;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute.
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrh.
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.129300.
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T.
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., He.
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Le.
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Sch.
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J.
RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a larg
RT effort to identify novel human secreted and transmembran
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature020
RA Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashu.
RA Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E.
RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscou
RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.
RA Babbage A.K., Bagguley C.L., Bailey J., Banerjee R., Barl
RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O
RA Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown
RA Burford D.C., Burrill W., Burton J., Carder C., Carter N
RA Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S.,
RA Collier R.E., Collins J.E., Colman L.K., Corby N.R., Cov.
RA Culley K.M., Dhami P., Davies J., Dunn M., Earthrowl M.E
RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., F.
RA Frankland J., French L., Garner P., Garnett J., Ghorl M.
RA Gilby L.M., Gillson C.J., Glithero R.J., Grafham D.V., G.
RA Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Hal.
RA Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcot
RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle
RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M.,
RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K.

RA Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R.,
 RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi
 RA Maslen G.L., Matthews L., McCann O.T., McLaren S.J., McL.
 RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Ni
 RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Pa
 RA Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S.
 RA Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T.
 RA Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M.,
 RA Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G.,
 RA Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans
 RA Wall M., Wallis J.M., West A.P., White S.S., Whitehead S
 RA Whittaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.
 RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulso
 RA Durbin R.M., Hubbard T., Sulston J.E., Dunham I., Rogers
 RT "The DNA sequence and analysis of human chromosome 6.";
 RL Nature 425:805-811(2003).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2
 RC TISSUE=Eye;
 RX PubMed=15489334; DOI=10.1101/gr.2596504;
 RG The MGC Project Team;
 RT "The status, quality, and expansion of the NIH full-leng
 RT project: the Mammalian Gene Collection (MGC).";
 RL Genome Res. 14:2121-2127(2004).
 CC -!- SUBCELLULAR LOCATION: Membrane; Single-pass type I m
 CC protein (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q6UY11-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q6UY11-2; Sequence=VSP_011767;
 CC Note=Splicing acceptor site not canonical. No expe
 CC confirmation available;
 CC -!- SIMILARITY: Contains 6 EGF-like domains.
 CC -----
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 CC -----
 DR EMBL; [AY358126](#); [AAQ88493.1](#); -; mRNA.
 DR EMBL; [AL359813](#); [CAI23224.1](#); -; Genomic_DNA.
 DR EMBL; [BC000230](#); [AAH00230.1](#); -; mRNA.
 DR EMBL; [BC006425](#); [AAH06425.1](#); -; mRNA.
 DR EMBL; [BC110320](#); [AAI10321.1](#); -; mRNA.
 DR RefSeq; [NP_076421.2](#); -.
 DR RefSeq; [NP_996262.1](#); -.
 DR UniGene; [Hs.337251](#); -.
 DR Ensembl; [ENSG00000171462](#); Homo sapiens.
 DR GeneID; [65989](#); -.
 DR KEGG; [hsa:65989](#); -.
 DR H-InvDB; [MIX0005904](#); -.
 DR HGNC; HGNC:21113; DLK2.
 DR PharmGKB; [PA134922184](#); -.
 DR HOGENOM; Q6UY11; -.
 DR HOVERGEN; Q6UY11; -.
 DR CleanEx; [HS_DLK2](#); -.
 DR GermOnline; [ENSG00000171462](#); Homo sapiens.
 DR InterPro; [IPR006210](#); EGF.
 DR InterPro; [IPR000152](#); EGF-type_Asp/Asn_hydroxyl_CS.
 DR InterPro; [IPR001438](#); EGF_2.
 DR InterPro; [IPR000742](#); EGF_3.
 DR InterPro; [IPR001881](#); EGF_Ca_bd.
 DR InterPro; [IPR000000](#); EGF_1-like

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DR   InterPro; IPR000203; EGF_like.
DR   InterPro; IPR013032; EGF_like_reg_CS.
DR   Pfam; PF00008; EGF; 5.

DR   PRINTS; PF00010; EGFBLOOD.
DR   SMART; SM00181; EGF; 3.
DR   SMART; SM00179; EGF_CA; 2.
DR   PROSITE; PS00010; ASX_HYDROXYL; 2.
DR   PROSITE; PS00022; EGF_1; 6.
DR   PROSITE; PS01186; EGF_2; 6.
DR   PROSITE; PS50026; EGF_3; 6.
DR   PROSITE; PS01187; EGF_CA; 2.
PE   2: Evidence at transcript level;
KW   Alternative splicing; Calcium; EGF-like domain; Glycoprotein;
KW   Membrane; Repeat; Signal; Transmembrane.
FT   SIGNAL          1         26       Potential.
FT   CHAIN           27        383      Delta-like protein 2.
FT                                     /FTId=PRO\_0000007534.
FT   TOPO_DOM        27        306      Extracellular (Potential).
FT   TRANSMEM        307        327      Potential.
FT   TOPO_DOM        328        383      Cytoplasmic (Potential).
FT   DOMAIN          27         58      EGF-like 1.
FT   DOMAIN          62         89      EGF-like 2.
FT   DOMAIN          91        129      EGF-like 3.
FT   DOMAIN         131        172      EGF-like 4.
FT   DOMAIN         174        210      EGF-like 5; calcium-binding
FT   DOMAIN         212        248      EGF-like 6; calcium-binding
FT   CARBOHYD        157        157      N-linked (GlcNAc...) (Poten
FT   DISULFID         29         40      By similarity.
FT   DISULFID         33         46      By similarity.
FT   DISULFID         48         57      By similarity.
FT   DISULFID         66         71      By similarity.
FT   DISULFID         79         88      By similarity.
FT   DISULFID         95        107      By similarity.
FT   DISULFID        101        117      By similarity.
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FT   DISULFID        162        171      By similarity.
FT   DISULFID        178        189      By similarity.
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FT   DISULFID        216        227      By similarity.
FT   DISULFID        221        236      By similarity.
FT   DISULFID        238        247      By similarity.
FT   VAR_SEQ          1         179      Missing (in isoform 2).
FT                                     /FTId=VSP\_011767.
SQ   SEQUENCE 383 AA; 40548 MW; 701AC6B043863EA7 CRC64;
      MP SGCRCLHL VCLLCILGAP GQVVRADDCS SHCDLAHGCC APDGSCRCDP G
      VRMPGCQHGT CHQPWQCICH SGWAGKFCDK DEHICTTQSP CQNGGQCMYD G
      PGFHGRDCER KAGPCEQAGS PCRNGGQCQD DQGFALNFTC RCLVGFVGAR C
      RPCANGATCL DGINRFSCLC PEGFAGRFT INLDDCASRP CQRGARCRDR V
      GYGKKTCELV LPVPDPPTTV DTPLGPTSAV VVPATGPAPH SAGAGLLRIS V
      GLGEP SLVAL VVFGALTAAL VLATVLLTLR AWRRGVCP PG PCCYPAPHYA P
      SMLPAGLPLP RDL PPEPGKT TAL
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